

11	20	38	47	56
5' GAGGC AAG AAT TCG GCA CGA GGC TCA GCT CCG CAC CGC AAC TGA AGA TCT GCC GCC				
65	74	83	92	101
GGC GAA CAG TTG CGT CTC CAT CTG GCT ACC AAC CCA CCC AAG CTT TCT TCT CCA				
119	128	137	146	155
CCA CCA CCA CCT TCC CTT CCC CCT CCT CCC CCT TTC GGT CCT CCC TCT				
173	182	191	200	209
CCA CCC CCG CCC CCA ATC TCC TCC TTT TTT TCT CAC TAC GAG CGG TTG CTG ATG M				
227	236	245	254	263
CTG AAG CCG AGC GTC ACT TCG GCT CCC ACG GCA GAC ATG GCG ACA TTG ACA GTG				
L K P S V T S A P T A D M A T L T V				
281	290	299	308	317
GTC CAG CCG CTC ACC CTG GAC AGA GAT GTT GCA AGA GCA ATT GAA TTA CTG GAA				
V Q P L T L D R D V A R A I E L L E				
335	344	353	362	371
AAA CTA CAG GAA TCT GGA GAA GTA CCA CTG CAC AAG CTA CAA TCC CTC AAA AAA				
K L Q E S G E V P V H K L Q S L K K				
389	398	407	416	425
GTG CTT CAG AGT GAG TTT TGT ACA GCT ATT CGA GAG GTG TAT CAA TAT ATG CAT				
V L Q S E F C T A I R E V Y Q Y M H				

FIGURE 1A

443	GAA	ACG	ATA	ACT	GTT	AAT	GGC	CCC	GAA	TTC	CGT	CGC	AGG	GCA	ACA	GCA	AAG	488	
	E	T	I	T	V	N	G	C	P	E	F	R	A	R	A	T	A	K	
452																		479	
461																			
497	GCA	ACA	GTT	GCA	GCT	TTT	GCA	GCT	AGT	GAA	GGC	CAC	TCC	CAC	CCT	CGA	GTA	GTT	542
	A	T	V	A	A	F	A	A	S	E	G	H	S	H	P	R	V	V	
506																			533
515																			
551	GAA	CTG	CCA	AAG	ACT	GAT	GAA	GGC	CTT	GGT	TTT	AAT	GTG	ATG	GGA	GGA	AAG	GAG	596
	E	L	P	K	T	D	E	G	L	G	F	N	V	M	G	G	K	E	
560																			587
569																			
605	CAA	AAT	TCC	CCC	ATT	TAT	ATC	TCCT	CGC	ATA	ATT	CCT	GGA	GGG	GTG	GCT	GAA	AGA	650
	Q	N	S	P	I	Y	I	S	R	I	I	P	G	G	V	A	E	R	
614																			641
623																			
659	CAC	GGA	GGC	CTC	AAA	AGA	GGA	GAC	CAG	CTG	CTA	TCA	GTG	AAC	GGA	GTG	AGT	GTG	704
	H	G	G	L	K	R	G	D	Q	L	L	S	V	N	G	V	S	V	
668																			695
677																			
713	GAA	GGA	GAA	CAC	CAT	GAG	AAA	GCT	GTG	GAA	CTA	CTC	AAG	GCT	GCT	AAA	GAC	AGC	758
	E	G	E	H	H	E	K	A	V	E	L	L	K	A	A	K	D	S	
722																			749
731																			
767	GTC	AAG	CTG	GTG	GTG	CGA	TAC	ACC	CCA	AAA	GTT	CTG	GAA	GAA	ATG	GAG	GCT	CGC	812
	V	K	L	V	V	R	Y	T	P	K	V	L	E	E	M	E	A	R	
776																			803
785																			

FIGURE 1B

821	830	839	848	857	866
TTT GAA AAG CTA CGA ACA GCC AGG CGT CGG CAG CAG CAA TTG CTA ATT CAG					
F E K L R T A R R R Q Q Q Q L L I Q					
875	884	893	902	911	920
CAG CAG CAA CAG CAG CAG CAA CAA ACA CAA AAC CAC ATG TCA TAG GCC					
Q Q Q Q Q Q Q Q T Q Q N H M S					
929	938	947	956	965	974
CTT GAG GGA AAG CTA CTT GAT CAA ACA TCC GAT AGT CAC AAA TTT GAA ACC GTG					
983	992	1001	1010	1019	1028
CTT CAG AAT CCC AGC ACA TAG TAA AAG ACA ACA CTG ATA ATT ATA CCT GTC AAG					
1037	1046	1055	1064	1073	1082
AAG CTG TGA ACA CAT GGT GTA TAA ATT CTT TAC CAA GGC AAC TCA ACA CCT TCT					
1091	1100	1109	1118	1127	1136
TTC TCT GGG CTT GAA CCG CCA CTG CTC ACG TGG GCT TTA CAT ACA TTG ACC TTC					
1145	1154	1163	1172	1181	1190
CAT TCA CTG CAG TGG GAA TTC TCA GTG TGC AGA GGG AGA GGT TTT CTA GTC TGC					
1199	1208	1217	1226	1235	1244
AAA CTG AAA CAG TGT AAG AAG AAT AAA GTC TAT GAC TTT TAA ATA AAA AAA AAA 3'					

FIGURE 1C

25 LDRDVARAIELLEKLOESGEVPVHKLQSLK 1974337  
 117 LERDVQRILELMEHVQKTKTEVNNAKLASLQ GI 1685067

55 KVLQSEFC TAIREVYQYMHETITVNGCPEF 1974337  
 147 QVLQSEFC AVREVEYETVYESI DADTPEI GI 1685067

85 RARATAKATVAAF AASEGHSHPRVVELPKT 1974337  
 177 KAAATAKATVAAF AAEHGHAPHRIVELPKT GI 1685067

115 DEGLGFNVMGKKEQNSPIYISRIIPGGVAE 1974337  
 207 DQGLGFNVMGKKEQNSPIYISRIIPGGVAD GI 1685067

145 RHGGLKRGDQLLSVNGVSEGEHHEKAVEL 1974337  
 237 RHGGLKRGDQLIAVNG-NVEAECH EKAVDL GI 1685067

175 LKA AKDSVKLVVRYTPKVL EEMEERFERQR 1974337  
 266 LKSAVGSVKLVIRYMPKLLDEMEERFERQR GI 1685067

FIGURE 2